

## SEQUENCE LISTING

<110> Ecole Polytechnique Fédérale de Lausanne (EPFL)

<120> Method for identification of suitable fragmentation sites in a reporter protein

<130> PEPF001WO

<150> US 34,404 JM-213

<151> 2003-10-09

<160> 66

<170> PatentIn version 3.1

<210> 1

<211> 672

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> modified base

<222> (186)..(186)

<223> silent point mutation introduced to generate HindIII restriction site

<300>

<308> NCBI / NC\_001136

<309> 2004-08-30

<400> 1

atgtctgtta ttaatttcac aggtagttct ggtccattgg tgaaagtttg cggcttgcag	60
agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt	120
gtgcccaata gaaagagaac aattgacccg gttattgcaa ggaaaatttc aagtcttgta	180
aaagcatata aaaatagttc aggcactccg aaatacttgg ttggcgtggt tcgtaataca	240
cctaaggagg atgttttggc tctgggtcaat gattacggca ttgatatcgt ccaactgcac	300
ggagatgagt cgtggcaaga ataccaagag ttctctgggt tgccagttat taaaagactc	360
gtattttcaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcgttt	420
attcccttgt ttgattcaga agcagggtggg acagggtgaac ttttggattg gaactcgatt	480
tctgactggg ttggaaggca agagagcccc gagagcttac attttatggt agctggtgga	540
ctgacgccag aaaatgttgg tgatgcgctt agattaaatg gcgttattgg tgttgatgta	600
agcggaggtg tggagacaaa tgggtgtaaaa gactctaaca aaatagcaaa tttcgtcaaa	660
aatgctaaga aa	672

<210> 2

<211> 224

<212> PRT

<213> *Saccharomyces cerevisiae*

&lt;300&gt;

&lt;308&gt; NCBI / NC\_001136

&lt;309&gt; 2004-08-30

&lt;400&gt; 2

Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val  
1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp  
20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile  
35 40 45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys  
50 55 60

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln  
65 70 75 80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile  
85 90 95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu  
100 105 110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile  
115 120 125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe  
130 135 140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile  
145 150 155 160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met  
165 170 175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu  
180 185 190

Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val Glu Thr Asn Gly  
195 200 205

Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys  
210 215 220

&lt;210&gt; 3

<211> 132  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<220>  
 <221> modified\_base  
 <222> (22)..(22)  
 <223> point mutation

<400> 3  
 atgtctgtta ttaatttcac atgtagttct ggtccattgg tgaaagtttg cggcttgacg 60  
 agcacagagg cgcgagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120  
 gtgccaata ga 132

<210> 4  
 <211> 44  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 4

Met Ser Val Ile Asn Phe Thr Cys Ser Ser Gly Pro Leu Val Lys Val  
 1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp  
 20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg  
 35 40

<210> 5  
 <211> 540  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 5  
 aagagaacaa ttgaccoggt tattgcaagg aaaatttcaa gtcttgtaaa agcatataaa 60  
 aatagttcag gcactccgaa atacttggtt ggcgtgtttc gtaatcaacc taaggaggat 120  
 gttttggctc tgggtcaatga ttacggcatt gatatogtcc aactgcacgg agatgagtcg 180  
 tggcaagaat accaagagtt cctcggtttg ccagttatta aaagactcgt atttccaaaa 240  
 gactgcaaca tactactcag tgcagcttca cagaaacctc attcgtttat tcccttggtt 300  
 gattcagaag caggtgggac aggtgaactt ttggattgga actcgatttc tgactggggtt 360  
 ggaaggcaag agagccccga gagcttacat tttatgttag ctggtggact gacgccagaa 420  
 aatgttggtg atgcgcttag attaaatggc gttattggtg ttgatgtaag cggaggtgtg 480  
 gagacaaatg gtgtaaaaga ctctaacaaa atagcaaatt tcgtcaaaaa tgctaagaaa 540

<210> 6

<211> 180  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 6

Lys Arg Thr Ile Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val  
 1 5 10 15

Lys Ala Tyr Lys Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val  
 20 25 30

Phe Arg Asn Gln Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr  
 35 40 45

Gly Ile Asp Ile Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr  
 50 55 60

Gln Glu Phe Leu Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys  
 65 70 75 80

Asp Cys Asn Ile Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe  
 85 90 95

Ile Pro Leu Phe Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp  
 100 105 110

Trp Asn Ser Ile Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser  
 115 120 125

Leu His Phe Met Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp  
 130 135 140

Ala Leu Arg Leu Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val  
 145 150 155 160

Glu Thr Asn Gly Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val Lys  
 165 170 175

Asn Ala Lys Lys  
 180

<210> 7  
 <211> 159  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 7  
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 agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120

gtgccaata gaaagagaac aattgacccg gttattgca

159

&lt;210&gt; 8

&lt;211&gt; 53

&lt;212&gt; PRT

&lt;213&gt; Saccharomyces cerevisiae

&lt;400&gt; 8

Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val  
1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp  
20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile  
35 40 45

Asp Pro Val Ile Ala  
50

&lt;210&gt; 9

&lt;211&gt; 516

&lt;212&gt; DNA

&lt;213&gt; Saccharomyces cerevisiae

&lt;400&gt; 9

gcaaggaaaa tttcaagtct tgtaaaagct tataaaaata gttcaggcac tccgaaatac 60  
ttggttggcg tgtttcgtaa tcaacctaag gaggatgttt tggctctggt caatgattac 120  
ggcattgata tcgtccaact gcacggagat gagtcgtggc aagaatacca agagttcctc 180  
ggtttgccag ttattaaaaag actcgtattt ccaaaagact gcaacatact actcagtgc 240  
gcttcacaga aacctcattc gtttattccc ttgtttgatt cagaagcagg tgggacaggt 300  
gaacttttgg attggaactc gatttctgac tgggttgga ggcaagagag ccccgagagc 360  
ttacatttta tgtagctgg tggactgacg ccagaaaatg ttggtgatgc gcttagatta 420  
aatggcgtta ttggtgttga tgtaagcgga ggtgtggaga caaatggtgt aaaagactct 480  
aacaaaatag caaatttcgt caaaaatgct aagaaa 516

&lt;210&gt; 10

&lt;211&gt; 172

&lt;212&gt; PRT

&lt;213&gt; Saccharomyces cerevisiae

&lt;400&gt; 10

Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys Asn Ser Ser Gly  
1 5 10 15

Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln Pro Lys Glu Asp  
20 25 30

Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile Val Gln Leu His  
35 40 45

Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu Gly Leu Pro Val  
50 55 60

Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile Leu Leu Ser Ala  
65 70 75 80

Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe Asp Ser Glu Ala  
85 90 95

Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile Ser Asp Trp Val  
100 105 110

Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met Leu Ala Gly Gly  
115 120 125

Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu Asn Gly Val Ile  
130 135 140

Gly Val Asp Val Ser Gly Gly Val Glu Thr Asn Gly Val Lys Asp Ser  
145 150 155 160

Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys  
165 170

<210> 11

<211> 561

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 11

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agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120  
gtgcccaata gaaagagaac aattgacccg gttattgcaa ggaaaatttc aagtcttgta 180  
aaagcttata aaaatagttc aggcactccg aaatacttgg ttggcgtgtt tcgtaatcaa 240  
cctaaggagg atgttttggc tctggtcaat gattacggca ttgatatcgt ccaactgcac 300  
ggagatgagt cgtggcaaga ataccaagag ttctctgggt tgccagttat taaaagactc 360  
gtatttccaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcgttt 420  
attcccttgt ttgattcaga agcaggtggg acaggtgaac ttttggattg gaactcgatt 480  
tctgactggg ttggaaggca agagagcccc gagagcttac attttatgtt agctggtgga 540

ctgacgccag aaaatgttgg t

561

&lt;210&gt; 12

&lt;211&gt; 187

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 12

Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val  
 1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp  
 20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile  
 35 40 45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys  
 50 55 60

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln  
 65 70 75 80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile  
 85 90 95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu  
 100 105 110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile  
 115 120 125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe  
 130 135 140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile  
 145 150 155 160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met  
 165 170 175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly  
 180 185

&lt;210&gt; 13

&lt;211&gt; 111

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

<400> 13  
 gatgcgctta gattaaatgg cgttattggt gttgatgtaa gcggaggtgt ggagacaaat 60  
 ggtgtaaaag actctaacaa aatagcaaat ttcgtcaaaa atgctaagaa a 111

<210> 14  
 <211> 37  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 14  
 Asp Ala Leu Arg Leu Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly  
 1 5 10 15

Val Glu Thr Asn Gly Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val  
 20 25 30

Lys Asn Ala Lys Lys  
 35

<210> 15  
 <211> 612  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<220>  
 <221> mutation  
 <222> (22)..(22)  
 <223> point mutation

<220>  
 <221> deletion  
 <222> (612)..(612)  
 <223> missing sequence after base 612 of wild-type: GAGACAAATGGTGTAAAAG  
 ACTCT

<400> 15  
 atgtctgtta ttaatttcac atgtagttct ggtccattgg tgaaagtttg cggcttgcag 60  
 agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120  
 gtgcccaata gaaagagaac aattgacccg gttattgcaa ggaaaatttc aagtcttgta 180  
 aaagcttata aaaatagttc aggcactccg aaatacttgg ttggcgtggt tcgtaatcaa 240  
 cctaaggagg atgttttggc tctgggtcaat gattacggca ttgatatcgt ccaactgcac 300  
 ggagatgagt cgtggcaaga ataccaagag ttcctcgggt tgccagttat taaaagactc 360  
 gtattttcaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcgttt 420  
 attcccttgt ttgattcaga agcaggtggg acaggtgaac ttttggattg gaactcgatt 480  
 tctgactggg ttggaaggca agagagcccc gagagcttac attttatgtt agctggtgga 540



9/20

ctgacgccag aaaatgttgg tgatgcgctt agattaaatg gcgttattgg tgttgatgta 600  
 agcggaggtg tg 612

<210> 16  
 <211> 204  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 16

Met Ser Val Ile Asn Phe Thr Cys Ser Ser Gly Pro Leu Val Lys Val  
 1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp  
 20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile  
 35 40 45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys  
 50 55 60

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln  
 65 70 75 80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile  
 85 90 95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu  
 100 105 110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile  
 115 120 125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe  
 130 135 140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile  
 145 150 155 160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met  
 165 170 175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu  
 180 185 190

Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val  
 195 200

<210> 17  
 <211> 36  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*  
  
 <220>  
 <221> mutation  
 <222> (1)..(1)  
 <223> missing sequence before base 1 of SEQ17, corresponding to base 63  
 7 of wild-type: GAGACAAATGGTGTAAGACTCT

<400> 17  
 aacaaaatag caaatttcgt caaaaatgct aagaaa 36

<210> 18  
 <211> 12  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 18

Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys  
 1 5 10

<210> 19  
 <211> 43  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> first of a pair of peptides (together with peptide C2), that asso-  
 ciate into an anti-parallel coiled coil (Biochemistry 37 (1998),  
 12603-12610)

<400> 19

Met Asp Tyr Lys Asp Glu Ser Gly Gln Ala Leu Glu Lys Glu Leu Ala  
 1 5 10 15

Gln Asn Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Leu  
 20 25 30

Glu Lys Glu Leu Gln Ala Gly Ser Gly Ser Gly  
 35 40

<210> 20  
 <211> 50  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> second of a pair of peptides (together with peptide C1), that ass-  
 ociate into an anti-parallel coiled coil (Biochemistry 37 (1998),  
 12603-12610)

<400> 20

Gly Gly Ser Gly Ser Gly Gln Ala Leu Lys Lys Lys Leu Ala Gln Leu  
 1 5 10 15

Lys Trp Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Lys  
 20 25 30

Lys Leu Gln Ala Gly Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ala  
 35 40 45

Phe Leu  
 50

<210> 21  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer for Ctrp fusions

<400> 21  
 cgatacgaat tcatggacaa ggattgtgaa atgaaacgc 39

<210> 22  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer for pRS316-C1/2CUP1

<400> 22  
 aaaggaattg gcccaaatg agtgggagtt acaagcactt gagaa 45

<210> 23  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer for pRS316-C1/2CUP1

<400> 23  
 ctcaatgttc gtgaactctt cctcgagcga gttgaactct tcctc 45

<210> 24  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer for pRS316-C1/2CUP1

<400> 24  
 ctccttctca agttgagcga gtccttctc aagtgcttgt aactc 45

<210> 25  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer for pRS316-C1/2CUP1

<400> 25  
ggcacttaag aagaagttgg cgcagcttaa gtggaaactg ca 42

<210> 26  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer for pRS316-C1/2CUP1

<400> 26  
agctgggcat tcttcttctt aagagcttgc agtttccact taagct 46

<210> 27  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer for pRS316-C1/2CUP1

<400> 27  
aagaagaaga atgcccagct taagaagaag ctccaggctg gaagttac 48

<210> 28  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer for pRS316-C1/2CUP1

<400> 28  
atacgatggt ccagattacg ctgcattttt ataagtcgac tggtc 45

<210> 29  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer for pRS316-C1/2CUP1

<400> 29  
gaccagtcga cttataaaaa tg 22

<210> 30

<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer for circular permutation of TRP1

<400> 30  
gtaaaagctt ataaaaatag ttcag 25

<210> 31  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer for circular permutation of TRP1

<400> 31  
gaaatagcct aggatgtctg ttattaattt cacagg 36

<210> 32  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer for circular permutation of TRP1

<400> 32  
cagacatcct aggctatttc ttagcathtt tgacg 35

<210> 33  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer for circular permutation of TRP1

<400> 33  
tttataagct tttacaagac ttgaa 25

<210> 34  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer for pRS316-C1/2CUP1

<400> 34  
gtaacgaatt catggactac aa 22

<210> 35  
<211> 66  
<212> DNA  
<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Primer for pRS316-C1/2CUP1

&lt;400&gt; 35

cattttgggc caattccttt tccagtgcct gaccactttc gtctttgtag tccatgaatt 60

cgttac

66

&lt;210&gt; 36

&lt;211&gt; 64

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Primer for pRS316-C1/2CUP1

&lt;400&gt; 36

caacttcttc ttaagtcct gacctgatcc agatccaccg ttaacacctg aacctgatcc 60

ggcc

64

&lt;210&gt; 37

&lt;211&gt; 43

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Primer for pRS316-C1/2CUP1

&lt;400&gt; 37

gtaatctgga acatcgatg ggtaacttcc agcctggagc ttc 43

&lt;210&gt; 38

&lt;211&gt; 66

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Primer for homologous recombination

&lt;400&gt; 38

gactctaaca aaatagcaaa ttctgtcaaa aatgctaaga aatagagggc cgcacatgt 60

aattag

66

&lt;210&gt; 39

&lt;211&gt; 65

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Primer for homologous recombination

&lt;400&gt; 39

aactttcacc aatggaccag aactacctgt gaaattaata acagacattt tgagatccgg 60

gtttt

65

<210> 40  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer for Ctrp fusions

<400> 40  
gcctgatcca gatccgcctt ctggtgattc atcatcttca 40

<210> 41  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer for Ctrp fusions

<400> 41  
ggcggatctg gatcaggcaa gagaacaatt gacccggtta 40

<210> 42  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer for Ctrp fusions

<400> 42  
gcctgatcca gatccgccta taaaagggtat tccgacacca 40

<210> 43  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer for Ntrp fusions

<400> 43  
gcctgatcca gatccgcctg caataaccgg gtcaattgt 39

<210> 44  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer for Ctrp fusions

<400> 44  
ggcggatctg gatcaggcgc aaggaaaatt tcaagtcttg 40

<210> 45  
<211> 42

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer for Ntrp fusions

<400> 45  
gcctgatcca gatccgccac caacattttc tggcgtcagt cc 42

<210> 46  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer for Ctrp fusions

<400> 46  
ggcggatctg gatcaggcga tgcgcttaga ttaaatggc 39

<210> 47  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer for Ntrp fusions

<400> 47  
gcctgatcca gatccgccca cacctccgct tacatcaac 39

<210> 48  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer for Ctrp fusions

<400> 48  
ggcggatctg gatcaggcaa caaaatag 28

<210> 49  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer for pRS315CUP1/ pRS316CUP1

<400> 49  
agcaggatcc cattaccgac atttg 25

<210> 50  
<211> 41  
<212> DNA  
<213> Artificial Sequence



<220>  
<223> Primer for pRS315CUP1/ pRS316CUP1

<400> 50  
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<210> 51  
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38